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PCT/EP99/04095

1

Sequence protocols

□

□

5 <110> Prof. Dr. Flügge, Ulf-Ingo

□

□

<120> DNA-sequence coding for a glucose-translocator

10 □

Plasmids, bacteria, yeasts and plants containing

□ said transporter

□

15

□

<130> plastidic glucose transporters

<140>

20 <141>

<150> 5652952

<151> 1999-06-13

25 <160> 6

<170> PatentIn Ver. 2.1

<210> 1

30 <211> 1874

<212> DNA

<213> Zea mays

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35 <221> CDS

<222> (2) .. (1630)

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&lt;222&gt; (1631)..(1874)

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5

10

15

tcg tgg agc ggc gat cgg aga ttg ccg gcg gtc aac ccc tgc agc gtg 97

10 Ser Trp Ser Gly Asp Arg Arg Leu Pro Ala Val Asn Pro Cys Ser Val

20

25

30

cgg atg ccg acg ggc aac gat ggg tgg tgc gcc ggc ctg agg tcg cgg 145

Arg Met Pro Thr Gly Asn Asp Gly Trp Cys Ala Gly Leu Arg Ser Arg

15

35

40

45

gcg gcg gat ctc gcc ggc ctc gag atg gcc aac ctg cgc ggc ggc gtc 193

Ala Ala Asp Leu Ala Gly Leu Glu Met Ala Asn Leu Arg Gly Gly Val

50

55

60

20

ggg ggg ctc ttc cgc gcg agc ccg cgc tac ggg cgc ttg caa gcc acg 241

Gly Gly Leu Phe Arg Ala Ser Pro Arg Tyr Gly Arg Leu Gln Ala Thr

65

70

75

80

25 gcg gca gtt gac cct gaa gat att cca ttg gag aag gtt caa gtt aaa 289

Ala Ala Val Asp Pro Glu Asp Ile Pro Leu Glu Lys Val Gln Val Lys

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90

95

tcc tca gga cat gtt ctg cca tat gtt ggc gtt gct tgt ttg ggg gct 337

30 Ser Ser Gly His Val Leu Pro Tyr Val Gly Val Ala Cys Leu Gly Ala

100

105

110

att ctg ttt ggt tac cat ctt ggt gtg gtc aat ggc gca ctt gaa tat 385

Ile Leu Phe Gly Tyr His Leu Gly Val Val Asn Gly Ala Leu Glu Tyr

35

115

120

125

ctc gcg aag gat ctt ggg att gct gaa aat gct gtc ttg cag ggg tgg 433

Leu Ala Lys Asp Leu Gly Ile Ala Glu Asn Ala Val Leu Gln Gly Trp

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	gtg gtt agc aca tcc ttg gct ggt gca aca cta ggt tct ttt act ggg 481			
	Val Val Ser Thr Ser Leu Ala Gly Ala Thr Leu Gly Ser Phe Thr Gly			
5	145	150	155	160
	ggg tct ttg gca gat aaa ttt ggg cgg aca aga aca ttc atc ctg gat 529			
	Gly Ser Leu Ala Asp Lys Phe Gly Arg Thr Arg Thr Phe Ile Leu Asp			
	165	170	175	
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	gca gtc cca ctt gct cta ggt gca ttc ttg agt gca aca gct caa gat 577			
	Ala Val Pro Leu Ala Leu Gly Ala Phe Leu Ser Ala Thr Ala Gln Asp			
	180	185	190	
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	gaa att cgt gga aca ctt ggt acc gtt aat caa ctt ttt att tgc att 721			
	Glu Ile Arg Gly Thr Leu Gly Thr Val Asn Gln Leu Phe Ile Cys Ile			
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	gga att ctt gca gct ttg tta gct gga ttg cct ctg gca gga aat cct 769			
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	245	250	255	
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	gcc tgg tgg agg aca atg ttt gga att gct gta gtt cca tcc att ctg 817			
	Ala Trp Trp Arg Thr Met Phe Gly Ile Ala Val Val Pro Ser Ile Leu			
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35	ctg gct gta gga atg gcc ttt tcg cct gaa agc cct cgt tgg cta ttc 865			
	Leu Ala Val Gly Met Ala Phe Ser Pro Glu Ser Pro Arg Trp Leu Phe			
	275	280	285	

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5 gga aaa gaa atg gtt acc gaa att atg ttt gat ctg aga gct agt ggc 961  
 Gly Lys Glu Met Val Thr Glu Ile Met Phe Asp Leu Arg Ala Ser Gly  
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caa agt tct tcg gag tcc gaa gcc ggc tgg ttt gat ctt ttc agc aag 1009  
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cgt tac tgg aaa gtt gtg agt gtg ggg gca gca ctg ttt ttg ttc cag 1057  
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20 cgt agt gca ggc att gca tct gat gtt gct gct agt gct ctt gtt gga 1153  
 Arg Ser Ala Gly Ile Ala Ser Asp Val Ala Ala Ser Ala Leu Val Gly  
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25 gca gcc aat gtt ttt ggt act atg gtt gca tct tct cta atg gac aaa 1201  
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 385 390 395 400

caa gga agg aaa agc ctt ctg ata aca agc ttt tct gga atg ggt gct 1249  
 30 Gln Gly Arg Lys Ser Leu Leu Ile Thr Ser Phe Ser Gly Met Gly Ala  
 405 410 415

tca atg cta ctc cta gca ttg tcc ttc acc tgg aaa gct ctg gca cct 1297  
 Ser Met Leu Leu Leu Ala Leu Ser Phe Thr Trp Lys Ala Leu Ala Pro  
 35 420 425 430

tat tct ggt act ctt gct gtt gtt ggc act gtt ctg tac gtg ctg tca 1345  
 Tyr Ser Gly Thr Leu Ala Val Val Gly Thr Val Leu Tyr Val Leu Ser

435                                      440                                      445  
 ttt gct cta gga gcg ggc cct gtt cca gcg cta ctt ctt cct gaa ata 1393  
 Phe Ala Leu Gly Ala Gly Pro Val Pro Ala Leu Leu Leu Pro Glu Ile  
 5            450                                      455                                      460  
 ttt gcc tcg aga ata agg gcc aag gct gtc gca tta tct cta ggc atg 1441  
 Phe Ala Ser Arg Ile Arg Ala Lys Ala Val Ala Leu Ser Leu Gly Met  
 465                                      470                                      475                                      480  
 10            cac tgg gta tct aac ttt ttc att ggc ctg tac ttc ctg agt gtc gtg 1489  
 His Trp Val Ser Asn Phe Phe Ile Gly Leu Tyr Phe Leu Ser Val Val  
 485                                      490                                      495  
 15            agc aag ttt ggg atc agc aac gtg tat ctg gga ttt gca tca gta tgt 1537  
 Ser Lys Phe Gly Ile Ser Asn Val Tyr Leu Gly Phe Ala Ser Val Cys  
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 gcc ctt gca gtt ctg tac ata gct ggg aat gtg gtc gag acc aag ggg 1585  
 20            Ala Leu Ala Val Leu Tyr Ile Ala Gly Asn Val Val Glu Thr Lys Gly  
 515                                      520                                      525  
 aga tca ctt gaa gag att gaa agg gag cta agt gta gca gaa tga 1630  
 Arg Ser Leu Glu Glu Ile Glu Arg Glu Leu Ser Val Ala Glu  
 25            530                                      535                                      540  
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 caaccgagca tccttgacc tggagactct ttctagtttc atgtagtttt agaaataagc 1750  
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 35            aaaa 1874

&lt;211&gt; 542

&lt;212&gt; PRT

&lt;213&gt; Zea mays

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Arg Met Pro Thr Gly Asn Asp Gly Trp Cys Ala Gly Leu Arg Ser Arg  
 35 40 45

15 Ala Ala Asp Leu Ala Gly Leu Glu Met Ala Asn Leu Arg Gly Gly Val  
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Gly Gly Leu Phe Arg Ala Ser Pro Arg Tyr Gly Arg Leu Gln Ala Thr  
 65 70 75 80

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Ala Ala Val Asp Pro Glu Asp Ile Pro Leu Glu Lys Val Gln Val Lys  
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Ser Ser Gly His Val Leu Pro Tyr Val Gly Val Ala Cys Leu Gly Ala  
 25 100 105 110

Ile Leu Phe Gly Tyr His Leu Gly Val Val Asn Gly Ala Leu Glu Tyr  
 115 120 125

30 Leu Ala Lys Asp Leu Gly Ile Ala Glu Asn Ala Val Leu Gln Gly Trp  
 130 135 140

Val Val Ser Thr Ser Leu Ala Gly Ala Thr Leu Gly Ser Phe Thr Gly  
 145 150 155 160

35

Gly Ser Leu Ala Asp Lys Phe Gly Arg Thr Arg Thr Phe Ile Leu Asp  
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Ala Val Pro Leu Ala Leu Gly Ala Phe Leu Ser Ala Thr Ala Gln Asp  
 180 185 190

Ile Arg Thr Met Ile Ile Gly Arg Leu Leu Ala Gly Ile Gly Ile Gly  
 5 195 200 205

Val Ser Ser Ala Leu Val Pro Leu Tyr Ile Ser Glu Ile Ser Pro Thr  
 210 215 220

10 Glu Ile Arg Gly Thr Leu Gly Thr Val Asn Gln Leu Phe Ile Cys Ile  
 225 230 235 240

Gly Ile Leu Ala Ala Leu Leu Ala Gly Leu Pro Leu Ala Gly Asn Pro  
 245 250 255

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Ala Trp Trp Arg Thr Met Phe Gly Ile Ala Val Val Pro Ser Ile Leu  
 260 265 270

Leu Ala Val Gly Met Ala Phe Ser Pro Glu Ser Pro Arg Trp Leu Phe  
 20 275 280 285

Gln Gln Gly Lys Val Thr Gln Ala Glu Leu Ala Val Lys Arg Leu Tyr  
 290 295 300

25 Gly Lys Glu Met Val Thr Glu Ile Met Phe Asp Leu Arg Ala Ser Gly  
 305 310 315 320

Gln Ser Ser Ser Glu Ser Glu Ala Gly Trp Phe Asp Leu Phe Ser Lys  
 325 330 335

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Arg Tyr Trp Lys Val Val Ser Val Gly Ala Ala Leu Phe Leu Phe Gln  
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Gln Leu Ala Gly Ile Asn Ala Val Val Tyr Tyr Ser Thr Ser Val Phe  
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Arg Ser Ala Gly Ile Ala Ser Asp Val Ala Ala Ser Ala Leu Val Gly  
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Ala Ala Asn Val Phe Gly Thr Met Val Ala Ser Ser Leu Met Asp Lys  
 385 390 395 400

5 Gln Gly Arg Lys Ser Leu Leu Ile Thr Ser Phe Ser Gly Met Gly Ala  
 405 410 415

Ser Met Leu Leu Leu Ala Leu Ser Phe Thr Trp Lys Ala Leu Ala Pro  
 420 425 430

10 Tyr Ser Gly Thr Leu Ala Val Val Gly Thr Val Leu Tyr Val Leu Ser  
 435 440 445

Phe Ala Leu Gly Ala Gly Pro Val Pro Ala Leu Leu Leu Pro Glu Ile  
 15 450 455 460

Phe Ala Ser Arg Ile Arg Ala Lys Ala Val Ala Leu Ser Leu Gly Met  
 465 470 475 480

20 His Trp Val Ser Asn Phe Phe Ile Gly Leu Tyr Phe Leu Ser Val Val  
 485 490 495

Ser Lys Phe Gly Ile Ser Asn Val Tyr Leu Gly Phe Ala Ser Val Cys  
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25 Ala Leu Ala Val Leu Tyr Ile Ala Gly Asn Val Val Glu Thr Lys Gly  
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Arg Ser Leu Glu Glu Ile Glu Arg Glu Leu Ser Val Ala Glu  
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<210> 3

35 <211> 1653

<212> DNA

<213> Solanum tuberosum



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&lt;221&gt; CDS

&lt;222&gt; (1)..(1419)

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&lt;221&gt; 3'UTR

&lt;222&gt; (1420)..(1653)

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gat gca gca cct ctc aaa gtt caa ggc caa tca tct gga tca gta ctt 96  
 15 Asp Ala Ala Pro Leu Lys Val Gln Gly Gln Ser Ser Gly Ser Val Leu  
 20 25 30

ccc tat gtg ggt gta gct tgt ctg gga gca att tta ttt gga tat cac 144  
 Pro Tyr Val Gly Val Ala Cys Leu Gly Ala Ile Leu Phe Gly Tyr His  
 20 35 40 45

cta ggg gtg gtg aat ggt gcc ctt gag tac cta gct aag gat ctt gga 192  
 Leu Gly Val Val Asn Gly Ala Leu Glu Tyr Leu Ala Lys Asp Leu Gly  
 50 55 60

25

att gcc gag aac act gtt ata caa gga tgg att gtt agc aca gtt ctt 240  
 Ile Ala Glu Asn Thr Val Ile Gln Gly Trp Ile Val Ser Thr Val Leu  
 65 70 75 80

30 gct ggc gcc ttt gtt ggt tca ttt act ggt gga gtt ctg gct gat aaa 288  
 Ala Gly Ala Phe Val Gly Ser Phe Thr Gly Gly Val Leu Ala Asp Lys  
 85 90 95

ttt ggc cga aca aag aca ttt ata ttg gat gca att cca ctt tca gtt 336  
 35 Phe Gly Arg Thr Lys Thr Phe Ile Leu Asp Ala Ile Pro Leu Ser Val  
 100 105 110

ggc gcg ttt cta tgt acc act gcc cag agt gtt cag gct atg atc att 384

Gly Ala Phe Leu Cys Thr Thr Ala Gln Ser Val Gln Ala Met Ile Ile  
 115 120 125

gga cgc tta ctt act gga att ggc att ggc atc tca tct gct att gtg 432  
 5 Gly Arg Leu Leu Thr Gly Ile Gly Ile Gly Ile Ser Ser Ala Ile Val  
 130 135 140

cca ctt tac ata tct gag atc tca ccc act gaa att cgc ggc aca ctg 480  
 Pro Leu Tyr Ile Ser Glu Ile Ser Pro Thr Glu Ile Arg Gly Thr Leu  
 10 145 150 155 160

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 165 170 175

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 gtg gtt gga ttg cct ttg tct gga aat cct tcg tgg tgg aga aca atg 576  
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 180 185 190

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 195 200 205

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 25 Phe Ser Pro Glu Ser Pro Arg Trp Leu Tyr Gln Gln Gly Arg Ile Ser  
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gaa gct gag aca tct att aaa agg cta tat ggt aaa gaa aaa gtt gct 720  
 Glu Ala Glu Thr Ser Ile Lys Arg Leu Tyr Gly Lys Glu Lys Val Ala  
 30 225 230 235 240

gag gtt atg ggt gac ttg gaa gct tct gcc cgg ggt tct tca gaa cca 768  
 Glu Val Met Gly Asp Leu Glu Ala Ser Ala Arg Gly Ser Ser Glu Pro  
 245 250 255

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 gat gct ggg tgg ctt gat cta ttt agt agc cgt tat agg aaa gtt gtt 816  
 Asp Ala Gly Trp Leu Asp Leu Phe Ser Ser Arg Tyr Arg Lys Val Val  
 260 265 270

agc att ggt gca gct atg ttc ttg ttg cag cag ttg gct ggg ata aat 864  
 Ser Ile Gly Ala Ala Met Phe Leu Leu Gln Gln Leu Ala Gly Ile Asn  
 275 280 285

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10 tct gat gta gca gcc agt gct ctg gtt gga gca gcc aac gtc ttt ggg 960  
 Ser Asp Val Ala Ala Ser Ala Leu Val Gly Ala Ala Asn Val Phe Gly  
 305 310 315 320

aca acg gtg gca tcc tct ttg atg gac aaa caa gga agg aag agt ctc 1008  
 15 Thr Thr Val Ala Ser Ser Leu Met Asp Lys Gln Gly Arg Lys Ser Leu  
 325 330 335

ttg ctc ata agc tat act gga atg gct gca tca atg atg ttg ctt tcc 1056  
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 20 340 345 350

ttg tca ttc act tgg aag gtc ctg act cca tat tct ggc aca ctg gct 1104  
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 370 375 380

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 Pro Val Pro Ala Leu Leu Leu Pro Glu Ile Phe Ala Ser Arg Ile Arg  
 385 390 395 400

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 405 410 415

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## 12

Phe Ile Gly Leu Tyr Phe Leu Ser Ile Val Thr Lys Phe Gly Ile Ser  
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 5 Thr Val Tyr Met Gly Phe Ala Leu Ser Cys Leu Val Ala Val Val Tyr  
 435 440 445  
 ata act ggt aat gtc gtg gag aca aag ggg cgg tca ctg gag gag ata 1392  
 Ile Thr Gly Asn Val Val Glu Thr Lys Gly Arg Ser Leu Glu Glu Ile  
 10 450 455 460  
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 Glu Arg Glu Leu Ser Pro Ala Ile  
 465 470  
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 20 tttctttgtac gtgggcatca tgaatcatgg aacattgtaa aaacatgtaa ctgttatgga 1619  
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 35 40 45

Leu Gly Val Val Asn Gly Ala Leu Glu Tyr Leu Ala Lys Asp Leu Gly  
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5 Ile Ala Glu Asn Thr Val Ile Gln Gly Trp Ile Val Ser Thr Val Leu  
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Ala Gly Ala Phe Val Gly Ser Phe Thr Gly Gly Val Leu Ala Asp Lys  
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10 Phe Gly Arg Thr Lys Thr Phe Ile Leu Asp Ala Ile Pro Leu Ser Val  
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Gly Ala Phe Leu Cys Thr Thr Ala Gln Ser Val Gln Ala Met Ile Ile  
 15 115 120 125

Gly Arg Leu Leu Thr Gly Ile Gly Ile Gly Ile Ser Ser Ala Ile Val  
 130 135 140

20 Pro Leu Tyr Ile Ser Glu Ile Ser Pro Thr Glu Ile Arg Gly Thr Leu  
 145 150 155 160

Gly Thr Val Asn Gln Leu Phe Ile Cys Ile Gly Ile Leu Val Ala Leu  
 165 170 175

25 Val Val Gly Leu Pro Leu Ser Gly Asn Pro Ser Trp Trp Arg Thr Met  
 180 185 190

Phe Gly Leu Ala Leu Ile Pro Ser Val Leu Leu Ala Ile Gly Met Ala  
 30 195 200 205

Phe Ser Pro Glu Ser Pro Arg Trp Leu Tyr Gln Gln Gly Arg Ile Ser  
 210 215 220

35 Glu Ala Glu Thr Ser Ile Lys Arg Leu Tyr Gly Lys Glu Lys Val Ala  
 225 230 235 240

Glu Val Met Gly Asp Leu Glu Ala Ser Ala Arg Gly Ser Ser Glu Pro

14

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	260	265	270
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	Ala Val Val Tyr Tyr Ser Thr Ala Val Phe Arg Ser Ala Gly Ile Thr		
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	Ser Asp Val Ala Ala Ser Ala Leu Val Gly Ala Ala Asn Val Phe Gly		
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15	Thr Thr Val Ala Ser Ser Leu Met Asp Lys Gln Gly Arg Lys Ser Leu		
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	Leu Leu Ile Ser Tyr Thr Gly Met Ala Ala Ser Met Met Leu Leu Ser		
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20	Leu Ser Phe Thr Trp Lys Val Leu Thr Pro Tyr Ser Gly Thr Leu Ala		
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	Val Leu Gly Thr Val Leu Tyr Val Leu Ser Phe Ser Leu Gly Ala Gly		
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	Pro Val Pro Ala Leu Leu Leu Pro Glu Ile Phe Ala Ser Arg Ile Arg		
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30	Ala Lys Ala Val Ala Leu Ser Leu Gly Val His Trp Ile Met Asn Phe		
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	Phe Ile Gly Leu Tyr Phe Leu Ser Ile Val Thr Lys Phe Gly Ile Ser		
	420	425	430
35	Thr Val Tyr Met Gly Phe Ala Leu Ser Cys Leu Val Ala Val Val Tyr		
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 30 Met Gln Ala Ser Thr Phe Met Val Lys Gly Asn Leu Gly Phe Glu Val  
 1 5 10 15

cag aac cgt aga gtg gct ggg ctt gct ggg ttg aaa ggg tta agc tca 156  
 Gln Asn Arg Arg Val Ala Gly Leu Ala Gly Leu Lys Gly Leu Ser Ser  
 35 20 25 30

atc cgt tcc aat aat cta agt ttt gtg aat gtt aat gac aat aat tat 204  
 Ile Arg Ser Asn Asn Leu Ser Phe Val Asn Val Asn Asp Asn Asn Tyr

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	gga ttt gca aga ttg ggt ctt gat cat gtc atg aag tcc tca ccc aag	300		
	Gly Phe Ala Arg Leu Gly Leu Asp His Val Met Lys Ser Ser Pro Lys			
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	Tyr Arg Ser Val Lys Ala Gln Ala Ala Ser Gly Gly Asp Leu Glu Asp			
	85	90	95	
15	gcc act cct gtc aaa tat caa ggc aaa tct tct gca tca gtg ttg ccg	396		
	Ala Thr Pro Val Lys Tyr Gln Gly Lys Ser Ser Ala Ser Val Leu Pro			
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	tat gtt ggt gtt gct tgt ttg gga gct att ttg ttt gga tat cac ctt	444		
20	Tyr Val Gly Val Ala Cys Leu Gly Ala Ile Leu Phe Gly Tyr His Leu			
	115	120	125	
	ggt gtg gta aat gga gct ctt gac tac cta tct gcg gat tta gct att	492		
	Gly Val Val Asn Gly Ala Leu Asp Tyr Leu Ser Ala Asp Leu Ala Ile			
25	130	135	140	
	gct ggc aat act gtt tta caa gga tgg gtt gtg agc ata tta ctt gct	540		
	Ala Gly Asn Thr Val Leu Gln Gly Trp Val Val Ser Ile Leu Leu Ala			
	145	150	155	160
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	Gly Ala Thr Val Gly Ser Phe Thr Gly Gly Ser Leu Ala Asp Lys Phe			
	165	170	175	
35	gga agg aca aag acc ttc cag tta gat gca att cct ctt gca ata gga	636		
	Gly Arg Thr Lys Thr Phe Gln Leu Asp Ala Ile Pro Leu Ala Ile Gly			
	180	185	190	



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 Ala Tyr Leu Cys Ala Thr Ala Gln Asn Val Gln Ile Met Met Ile Gly  
 195 200 205

5 cgt tta ctt tgt ggc att gga att ggc ata tca tct gcc tta gtt ccg 732  
 Arg Leu Leu Cys Gly Ile Gly Ile Gly Ile Ser Ser Ala Leu Val Pro  
 210 215 220

tta tac att tct gag att tcg cca act gaa att cga ggt gca ctt ggt 780  
 10 Leu Tyr Ile Ser Glu Ile Ser Pro Thr Glu Ile Arg Gly Ala Leu Gly  
 225 230 235 240

tct gtc aac cag ctt ttt ata tgc att ggt att ctt gcg gct ttg gtt 828  
 Ser Val Asn Gln Leu Phe Ile Cys Ile Gly Ile Leu Ala Ala Leu Val  
 15 245 250 255

gct gga ttg cct tta gca gga aac cct ttg tgg tgg agg aca atg ttt 876  
 Ala Gly Leu Pro Leu Ala Gly Asn Pro Leu Trp Trp Arg Thr Met Phe  
 260 265 270

20 ggt att gca aca gtt ccc tct gtt ctc ttg gct ctt ggg atg ggc ttc 924  
 Gly Ile Ala Thr Val Pro Ser Val Leu Leu Ala Leu Gly Met Gly Phe  
 275 280 285

25 tgt cca gaa agc cct agg tgg ctt ttt cag caa gga aaa att gtt gaa 972  
 Cys Pro Glu Ser Pro Arg Trp Leu Phe Gln Gln Gly Lys Ile Val Glu  
 290 295 300

gca gaa aag gcc gta gca gcc ctc tat gga aaa gaa agg gtt ccg gag 1020  
 30 Ala Glu Lys Ala Val Ala Ala Leu Tyr Gly Lys Glu Arg Val Pro Glu  
 305 310 315 320

gtg att aat gat ttg aga gca tct gtt caa ggt tct tct gaa cca gaa 1068  
 Val Ile Asn Asp Leu Arg Ala Ser Val Gln Gly Ser Ser Glu Pro Glu  
 35 325 330 335

gct ggc tgg ttt gat ctg ttc agt agc cgc tac agg aaa gtg gta agt 1116  
 Ala Gly Trp Phe Asp Leu Phe Ser Ser Arg Tyr Arg Lys Val Val Ser

	340	345	350	
	gtt ggt gct gca ctt ttc ttg ttc cag caa atg gca gga atc aat gct Val Gly Ala Ala Leu Phe Leu Phe Gln Gln Met Ala Gly Ile Asn Ala			1164
5	355	360	365	
	gtt gta tat tac tcc aca tct gta ttc cga agt gct gga att gca tca Val Val Tyr Tyr Ser Thr Ser Val Phe Arg Ser Ala Gly Ile Ala Ser			1212
	370	375	380	
10	gat gtt gcc gct agt gcc ctt gtt gga gca tca aat gtt att ggc act Asp Val Ala Ala Ser Ala Leu Val Gly Ala Ser Asn Val Ile Gly Thr			1260
	385	390	395	400
15	gct gtc gcc tct tct tta atg gac aag caa gga aga aag agc cta ctg Ala Val Ala Ser Ser Leu Met Asp Lys Gln Gly Arg Lys Ser Leu Leu			1308
	405	410	415	
	atg aca agt ttc tca gga atg gct gcc tca atg ttg ttg ctg tca cta Met Thr Ser Phe Ser Gly Met Ala Ala Ser Met Leu Leu Leu Ser Leu			1356
20	420	425	430	
	tcg ttc aca tgg aag gct cta gca cct tac tcg ggc aca ctt gcc gtt Ser Phe Thr Trp Lys Ala Leu Ala Pro Tyr Ser Gly Thr Leu Ala Val			1404
25	435	440	445	
	gtg gga act gtt tta tat gtc ctt tcc ttt tca ctt ggc gct ggt cct Val Gly Thr Val Leu Tyr Val Leu Ser Phe Ser Leu Gly Ala Gly Pro			1452
	450	455	460	
30	gtt cct gct ctt cta ctt cca gag atc ttc gca tcc aga atc cga gca Val Pro Ala Leu Leu Leu Pro Glu Ile Phe Ala Ser Arg Ile Arg Ala			1500
	465	470	475	480
35	aaa gca gtg gct ttg tca ctg gga atg cat tgg gcg tca aac ttc gta Lys Ala Val Ala Leu Ser Leu Gly Met His Trp Ala Ser Asn Phe Val			1548
	485	490	495	

## 19

att ggc ctt tat ttc tta agt gtg gtg acc aag ttt gga atc agc aaa 1596  
 Ile Gly Leu Tyr Phe Leu Ser Val Val Thr Lys Phe Gly Ile Ser Lys  
 500 505 510

5 gtg tat ttg ggg ttc gcg tca gtg tgt gtg ctt gcc gtg ttg tac ata 1644  
 Val Tyr Leu Gly Phe Ala Ser Val Cys Val Leu Ala Val Leu Tyr Ile  
 515 520 525

gct ggt aac gtt gtt gaa aca aaa gga cga tca ctt gag gaa ata gag 1692  
 10 Ala Gly Asn Val Val Glu Thr Lys Gly Arg Ser Leu Glu Glu Ile Glu  
 530 535 540

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 Leu Ala Leu Ser Pro Ala Val  
 15 545 550

atctatagag aattatgtta ataattcccg gatttaggag tttgatgcta gttttcatgc 1806

tcgttggcac attcatgtcc agacagttgt actatcaatg tcagaaattc ctcgtgcc 1864  
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 25 <213> Spinacia oleracea

<400> 6  
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 20 25 30

Ile Arg Ser Asn Asn Leu Ser Phe Val Asn Val Asn Asp Asn Asn Tyr  
 35 35 40 45

Lys Ser Asn Pro Cys Lys Leu Ser Cys Gly Ser Leu Ser Met Gly Ala  
 50 55 60

20

Gly Phe Ala Arg Leu Gly Leu Asp His Val Met Lys Ser Ser Pro Lys  
 65 70 75 80

5 Tyr Arg Ser Val Lys Ala Gln Ala Ala Ser Gly Gly Asp Leu Glu Asp  
 85 90 95

Ala Thr Pro Val Lys Tyr Gln Gly Lys Ser Ser Ala Ser Val Leu Pro  
 100 105 110

10

Tyr Val Gly Val Ala Cys Leu Gly Ala Ile Leu Phe Gly Tyr His Leu  
 115 120 125

Gly Val Val Asn Gly Ala Leu Asp Tyr Leu Ser Ala Asp Leu Ala Ile  
 15 130 135 140

Ala Gly Asn Thr Val Leu Gln Gly Trp Val Val Ser Ile Leu Leu Ala  
 145 150 155 160

20 Gly Ala Thr Val Gly Ser Phe Thr Gly Gly Ser Leu Ala Asp Lys Phe  
 165 170 175

Gly Arg Thr Lys Thr Phe Gln Leu Asp Ala Ile Pro Leu Ala Ile Gly  
 180 185 190

25

Ala Tyr Leu Cys Ala Thr Ala Gln Asn Val Gln Ile Met Met Ile Gly  
 195 200 205

Arg Leu Leu Cys Gly Ile Gly Ile Gly Ile Ser Ser Ala Leu Val Pro  
 30 210 215 220

Leu Tyr Ile Ser Glu Ile Ser Pro Thr Glu Ile Arg Gly Ala Leu Gly  
 225 230 235 240

35 Ser Val Asn Gln Leu Phe Ile Cys Ile Gly Ile Leu Ala Ala Leu Val  
 245 250 255

Ala Gly Leu Pro Leu Ala Gly Asn Pro Leu Trp Trp Arg Thr Met Phe

21

260

265

270

Gly Ile Ala Thr Val Pro Ser Val Leu Leu Ala Leu Gly Met Gly Phe  
 275 280 285

5

Cys Pro Glu Ser Pro Arg Trp Leu Phe Gln Gln Gly Lys Ile Val Glu  
 290 295 300

Ala Glu Lys Ala Val Ala Ala Leu Tyr Gly Lys Glu Arg Val Pro Glu  
 10 305 310 315 320

Val Ile Asn Asp Leu Arg Ala Ser Val Gln Gly Ser Ser Glu Pro Glu  
 325 330 335

15 Ala Gly Trp Phe Asp Leu Phe Ser Ser Arg Tyr Arg Lys Val Val Ser  
 340 345 350

Val Gly Ala Ala Leu Phe Leu Phe Gln Gln Met Ala Gly Ile Asn Ala  
 355 360 365

20

Val Val Tyr Tyr Ser Thr Ser Val Phe Arg Ser Ala Gly Ile Ala Ser  
 370 375 380

Asp Val Ala Ala Ser Ala Leu Val Gly Ala Ser Asn Val Ile Gly Thr  
 25 385 390 395 400

Ala Val Ala Ser Ser Leu Met Asp Lys Gln Gly Arg Lys Ser Leu Leu  
 405 410 415

30 Met Thr Ser Phe Ser Gly Met Ala Ala Ser Met Leu Leu Leu Ser Leu  
 420 425 430

Ser Phe Thr Trp Lys Ala Leu Ala Pro Tyr Ser Gly Thr Leu Ala Val  
 435 440 445

35

Val Gly Thr Val Leu Tyr Val Leu Ser Phe Ser Leu Gly Ala Gly Pro  
 450 455 460

Val Pro Ala Leu Leu Leu Pro Glu Ile Phe Ala Ser Arg Ile Arg Ala  
465 470 475 480

Lys Ala Val Ala Leu Ser Leu Gly Met His Trp Ala Ser Asn Phe Val  
5 485 490 495

Ile Gly Leu Tyr Phe Leu Ser Val Val Thr Lys Phe Gly Ile Ser Lys  
500 505 510

10 Val Tyr Leu Gly Phe Ala Ser Val Cys Val Leu Ala Val Leu Tyr Ile  
515 520 525

Ala Gly Asn Val Val Glu Thr Lys Gly Arg Ser Leu Glu Glu Ile Glu  
530 535 540

15

Leu Ala Leu Ser Pro Ala Val  
545 550